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The envelope glycoprotein gp41 from human immunodeficiency virus type 1 (HIV-1) is involved in membrane fusion and virus entry. It contains a functionally important leucine zipper-like heptad repeat region (residues 553-590). To investigate the solution structure and membrane-binding properties of this region, cysteine-substituted variants of a 38-residue peptide derived from the heptad repeat were synthesized and modified with nitroxide spin labels. Analytical equilibrium ultracentrifugation studies indicated it is primarily tetrameric in solution, in contrast to the protein gp160 which is a mixture of trimers and tetramers. Electron paramagnetic resonance (EPR) measurements indicated that the peptide was bound to vesicles containing 10 mol % negatively charged lipids. The peptides were bound parallel to the membrane surface, near the water-membrane interface, in a structure different from the solution structure, most likely as monomers. When Asp, Pro, or Ser was substituted for Ile at the core "a" position of the heptad repeat in the middle of the peptide, the coiled coil was destabilized. In addition, these peptides showed reduced membrane-binding affinities. Thus, mutations that destabilized coiled-coil formation also decreased membrane-binding propensity. These experimental results, taken with previous evidence, suggest two functions for the heptad repeat of gp41 after CD4 binding: (1) to form an extended coiled coil; (2) to provide a hydrophobic face that binds to the host-cell membrane, bringing the viral and cellular membranes closer and facilitating fusion.

PMID: 7577925 [PubMed - indexed for MEDLINE]

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